WE CLAIM:

1. A peptide having an amino acid sequence of:

N(H)(R')-X' Z'(CORE PEPTIDE) Z'' X''-CO-R''

in which:

a) N(H)(R') is the amino terminal, wherein R' is acetyl or hydrogen; and CO-R'' is the carboxyl terminal, wherein R'' is NH_2 or OH;

b) X' is present or absent, and, if present, is an L-amino acid or a di- or tripeptide of D or L-amino acids selected from the group consisting of Y, W, and F, provided that no amino acid is selected more than once;

c) X'' is present or absent, and if present, is an L-amino acid selected from the group of consisting of Y, W, F, I, L or a dipeptide of D or L-amino acids selected from the group consisting of L and I;

d) Z' and Z'' are amino acids that are linked to each other so that the peptide is a cyclic peptide; and

e) the CORE PEPTIDE is selected from the group of peptides consisting of

*-N-Q-+	*-N-Q-L-+
*-N-Q-L-I-+	*-N-Q-L-I-K-+
*-N-Q-I-+	*-N-Q-I-K-+
*-S-N-+	*-S-N-Q-L-+
*-S-N-Q-L-I-+	*-S-N-Q-L-I-K-+
*-S-N-Q-I-+	*-S-N-Q-I-K-+
*-N-S-N-+	*-N-S-N-Q-+
*-N-S-N-Q-L-+	*-N-S-N-Q-L-I-+
*-N-S-N-Q-L-I-K-+	*-N-S-N-Q-I-K-+
*-N-S-N-Q-I-+	
*-K-N-S-N-+	*-K-N-S-N-Q-+
*-K-N-S-N-Q-L-+	*-K-N-S-N-Q-L-I-+
*-K-N-S-N-Q-L-I-K-+	*-K-N-S-N-Q-I-+
*-K-N-S-N-Q-I-K-+	*-N-S-N-Q-I-+
*-E-N-K-+	*-E-N-K-E-+
*-E-N-K-E-A-+	*-L-E-N-K-+

*-L-E-N-K-E-+ *-L-E-N-K-E-A-+

*-K-L-E-N-K-+ *-K-L-E-N-K-E-+

*-K-L-E-N-K-E-A-+

*-S-G-Q-+ *-S-G-Q-V-+

*-S-G-Q-V-L-+ *-D-S-G-Q-+

*-D-S-G-Q-V-+ *-D-S-G-Q-V-L-+

*-S-D-S-G-Q-+ *-S-D-S-G-Q-V-+

*-S-D-S-G-Q-V-L-+ *-L-S-D-S-G-Q-+

*-L-S-D-S-G-Q-V-+ and *-L-S-D-S-G-Q-V-L-+,

wherein * and + designate the amino and carboxyl termini, respectively, and the single letters designate L-amino acids according to the single letter code or wherein * and + designate the carboxyl and amino termini, respectively and the single letters designate D-amino acids according to the single letter code.

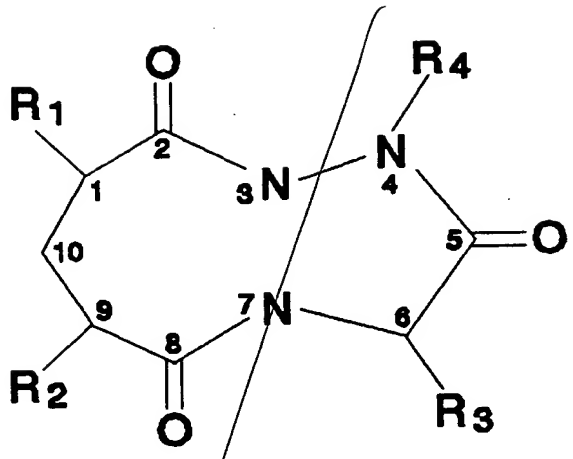
2. The peptide of claim 1, in which the CORE PEPTIDE is selected from the group consisting of *-K-N-S-N-Q-L-I-K-+, *-K-N-S-N-Q-I-K-+, *-N-S-N-Q-L-I-+, *-N-S-N-Q-I-+, *-L-S-D-S-G-Q-V-L-+, and *-K-L-E-N-K-E-A-+, wherein * and + designate the amino and carboxyl termini, respectively, and the single letters designate L-amino acids according to the single letter code, or wherein * and + designate the carboxyl and amino termini, respectively and the single letters designate D-amino acids according to the single letter code.

3. The peptide of claim 1, in which the CORE PEPTIDE is *-N-S-N-Q-I-+, wherein * and + designate the amino and carboxyl termini, respectively, and the single letters designate L-amino acids according to the single letter code.

4. The peptide of claim 3, which is CNSNQIC.

5. The peptide of claim 3, which is YCNSNQIC.

6. A macrocyclic peptidomimetic corresponding to a tetrameric, pentameric or hexameric peptide, having a 10-member ring according to the formula:



wherein:

R_1 is the α-carbon, amino moiety and side chain of the amino terminal amino acid of a tetrameric peptidomimetic or the amino terminal amino acid and the α-carbon, amine and side chain of the second amino acid of a pentameric or hexameric peptidomimetic;

R_2 is the side-chain of the second amino acid of a tetrameric or pentameric peptidomimetic or the side-chain of the third amino acid of a pentameric or hexameric peptidomimetic;

R_3 is the side chain of the third amino acid of a tetrameric or pentameric peptidomimetic or the fourth amino acid of a pentameric or hexameric peptidomimetic; and

R_4 and 4-N together are the carboxyl terminal amino acid of a tetrameric or pentameric peptidomimetic, or the carboxyl terminal two amino acids of a pentameric or hexameric peptidomimetic; and

the sequence of amino acids to which R_1 through R_4 correspond are selected from the following sequences:

*-N-Q-L-I-+
*-N-Q-I-K-+
*-S-N-Q-L-I-+
*-S-N-Q-I-+
*-N-Q-L-I-K-+
*-S-N-Q-L-+
*-S-N-Q-L-I-K-+
*-S-N-Q-I-K-+

*-N-S-N-Q-+
*-N-S-N-Q-L-I-+
*-N-S-N-Q-I-+
*-K-N-S-N-Q-+
*-K-N-S-N-Q-I-+
*-N-S-N-Q-I-+
*-E-N-K-E-A-+
*-L-E-N-K-E-+
*-K-L-E-N-K-+
*-S-G-Q-V-+
*-D-S-G-Q-+
*-D-S-G-Q-V-L-+
*-S-D-S-G-Q-V-+ and
*-N-S-N-Q-L-+
*-N-S-N-Q-I-K-+
*-K-N-S-N-+
*-K-N-S-N-Q-L-+
*-E-N-K-E-+
*-L-E-N-K-+
*-L-E-N-K-E-A-+
*-K-L-E-N-K-E-+
*-S-G-Q-V-L-+
*-D-S-G-Q-V-+
*-S-D-S-G-Q-+
*-L-S-D-S-G-Q-+,

wherein * denotes the amino terminal and + the carboxyl terminal.

7. The macrocyclic peptidomimetic of claim 6, in which the amino acids are selected from the sequences: *-N-S-N-Q-+, *-N-S-N-Q-I-+, wherein 4-N and R_4 together correspond to the C-terminal Q-I dipeptide, and *-K-N-S-N-Q-I-+.

8. A method of suppressing a human, CD4 T-cell immune response comprising administering to a subject having a medical condition that is ameliorated by the suppression of a CD4 T-cell mediated immune response, an effective amount of an active compound having a molecular weight of between 1450 daltons and about 400 daltons, which compound, at a concentration of at most 200 μM:

a) inhibits greater than 50% of the binding of human CD4-expressing, CD4-transfected COS cells to Raji cells; and

b) causes a less than 20% decrease in the growth of EB-transformed lymphoblastoid cells and IL-2-dependent HT-2 cells.

9. The method of claim 8, wherein the molecular weight of the active compound is less than 1400 daltons.

10. The method of claim 8, wherein the compound, at a concentration of at most 200 μM:

a) causes less than a 20% decrease in the response of human peripheral blood lymphocytes to lipopolysaccharide; and

b) inhibits greater than 25% of the response of a human mixed lymphocyte reaction.

11. The method of claim 10, wherein the molecular weight of the active compound is less than 1400 daltons.

12. The method of claim 11, wherein the medical condition is related to an allograft.

13. The method of claim 11, wherein the medical condition is multiple sclerosis.

14. The method of claim 11, wherein the active compound is a peptide or peptidomimetic.

15. The method of claim 14, wherein the active compound is a peptide according to the formula:

N(H)(R')-X' Z' A_1 A_2 A_3 A_4 A_5 A_6 A_7 A_8 Z'' X''-CO-R''

in which:

a) N(H)(R') is the amino terminal, wherein R' is acetyl or hydrogen; and CO-R'' is the carboxyl terminal, wherein R'' is NH_2 or OH;

b) A_1, A_2, A_3, A_4, A_5, A_6, A_7, and A_8 are chosen according to a scheme selected from the following schemes:

i. A_1 is K, R or H; A_2 is N, Q or D; A_3 is S, T, D or N; A_4 is N, D, E, or Q; A_5 is Q, N, E or M; A_6 is L, I, V or A; A_7 is I, L, V, or A; and A_8 is K, R or H;

ii. as in scheme (i) except that A_6 is omitted;

iii. as in scheme (ii) except that A_1 and A_8 are omitted;

iv. A_1 is K, R or H; A_2 is L, I, V or Q; A_3 is E, D or N; A_4 is N, Q or D; A_5 is K, R, H or Q; A_6 is E, D or N; A_7 is A, V or G; and A_8 is omitted; and

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v. A_1 is L, I or V; A_2 is S, T or D; A_3 is D, E or Q; A_4 is S, T, D or G; A_5 is G or D; A_6 is Q, N, E or K; A_7 is V, L or I; and A_8 is L, I, V or K,

wherein the single letters refer to L-amino acids in the single letter code;

c) X' is present or absent, and, if present, is an L-amino acid or a di- or tripeptide of D or L amino acids selected from the group consisting of Y, W, and F, provided that no amino acid is selected more than once;

d) X'' is present or absent, and if present, is a D or L-amino acid selected from the group of consisting of Y, W, F, I, L or a dipeptide of D or L-amino acids selected from the group consisting of L and I; and

e) Z' and Z'' are an amino acids that are linked to each other so that the peptide is a cyclic peptide.

16. The method of claim 14, wherein the active compound is a peptide according to the formula:

CO-R''-X'' Z' A_1 A_2 A_3 A_4 A_5 A_6 A_7 A_8 Z'' X'-N(H)(R')

in which:

a) N(H)(R') is the amino terminal, wherein R' is acetyl or hydrogen; and CO-R'' is the carboxyl terminal, wherein R'' is NH_2 or OH;

b) A_1, A_2, A_3, A_4, A_5, A_6, A_7, and A_8 are chosen according to a scheme selected from the following schemes:

i. A_1 is K, R or H; A_2 is N, Q or D; A_3 is S, T, D or N; A_4 is N, D, E, or Q; A_5 is Q, N, E or M; A_6 is L, I, V or A; A_7 is I, L, V, or A; and A_8 is K, R or H;

ii. as in scheme (i) except that A_6 is omitted;

iii. as in scheme (ii) except that A_1 and A_8 are omitted;

iv. A_1 is K, R or H; A_2 is L, I, V or Q; A_3 is E, D or N; A_4 is N, Q or D; A_5 is K, R, H or Q; A_6 is E, D or N; A_7 is A, V or G; and A_8 is omitted; and

v. A_1 is L, I or V; A_2 is S, T or D; A_3 is D, E or Q; A_4 is S, T, D or G; A_5 is G or D; A_6 is Q, N, E or K; A_7 is V, L or I; and A_8 is L, I, V or K,

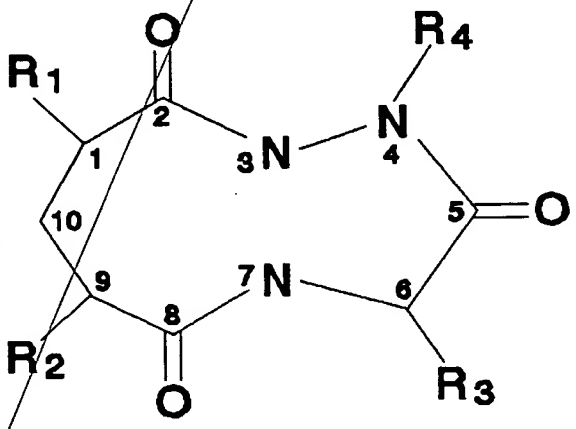
wherein the single letters refer to D-amino acids in the single letter code;

c) X' is present or absent, and, if present, is an L-amino acid or a di- or tripeptide of either D or L amino acids selected from the group consisting of Y, W, and F, provided that no amino acid is selected more than once;

d) X'' is present or absent, and if present, is a D or L-amino acid selected from the group of consisting of Y, W, F, I, L or a dipeptide of either D or L amino acids selected from the group consisting of L and I; and

e) Z' and Z'' are an amino acids that are linked to each other so that the peptide is a cyclic peptide.

17. The method of claim 14, wherein the active compound is a macrocyclic peptidomimetic corresponding to a tetrameric, pentameric or hexameric peptide, having a 10-member ring according to the formula:



wherein:

R_1 is the α-carbon, amino moiety and side chain of the amino terminal amino acid of a tetrameric peptidomimetic or the amino terminal amino acid and the α-carbon, amine and side chain of the second amino acid of a pentameric or hexameric peptidomimetic;

R_2 is the side-chain of the second amino acid of a

tetrameric or pentameric peptidomimetic or the side-chain of the third amino acid of a pentameric or hexameric peptidomimetic;

R_3 is the side chain of the third amino acid of a tetrameric or pentameric peptidomimetic or the fourth amino acid of a pentameric or hexameric peptidomimetic; and

R_4 and 4-N together are the carboxyl terminal amino acid of a tetrameric or pentameric peptidomimetic, or the carboxyl terminal two amino acids of a pentameric or hexameric peptidomimetic; and

the sequence of amino acids to which R_1 through R_4 correspond are selected from the following sequences:

*-N-Q-L-I-+
*-N-Q-I-K-+
*-S-N-Q-L-I-+
*-S-N-Q-I-+
*-N-S-N-Q-+
*-N-S-N-Q-L-I-+
*-N-S-N-Q-I-+
*-K-N-S-N-Q-+
*-K-N-S-N-Q-I-+
*-N-S-N-Q-I-+
*-E-N-K-E-A-+
*-L-E-N-K-E-+
*-K-L-E-N-K-+
*-S-G-Q-V-+
*-D-S-G-Q-+
*-D-S-G-Q-V-L-+
*-S-D-S-G-Q-V-+ and
*-N-Q-L-I-K-+
*-S-N-Q-L-+
*-S-N-Q-L-I-K-+
*-S-N-Q-I-K-+
*-N-S-N-Q-L-+
*-N-S-N-Q-I-K-+
*-K-N-S-N-+
*-K-N-S-N-Q-L-+

*-E-N-K-E-+
*-L-E-N-K-+
*-L-E-N-K-E-A-+
*-K-L-E-N-K-E-+
*-S-G-Q-V-L-+
*-D-S-G-Q-V-+
*-S-D-S-G-Q-+
*-L-S-D-S-G-Q-+,

wherein * denotes the amino terminal and + the carboxyl terminal.

18. A method of suppressing a human, CD4 T-cell immune response comprising administering to a subject having a medical condition that is ameliorated by the suppression of a CD4 T-cell mediated immune response, an effective amount of a peptide having an amino acid sequence of:

N(H)(R')-X' Z'(CORE PEPTIDE) Z'' X''-CO-R''

in which:

a) N(H)(R') is the amino terminal, wherein R' is acetyl or hydrogen; and CO-R'' is the carboxyl terminal, wherein R'' is NH_2 or OH;

b) X' is present or absent, and, if present, is an L-amino acid or a di- or tripeptide of D or L-amino acids selected from the group consisting of Y, W, and F, provided that no amino acid is selected more than once;

c) X'' is present or absent, and if present, is an L-amino acid selected from the group of consisting of Y, W, F, I, L or a dipeptide of D or L-amino acids selected from the group consisting of L and I;

d) Z' and Z'' are amino acids that are linked to each other so that the peptide is a cyclic peptide; and

e) the CORE PEPTIDE is selected from the group of peptides consisting of

*-N-Q-+
*-N-Q-L-I-+
*-N-Q-I-+
*-S-N-+
*-S-N-Q-L-I-+
*-S-N-Q-I-+
*-N-S-N-+
*-N-S-N-Q-L-+
*-N-S-N-Q-L-I-K-+
*-N-S-N-Q-I-+
*-K-N-S-N-+
*-K-N-S-N-Q-L-+
*-K-N-S-N-Q-L-I-K-+
*-K-N-S-N-Q-I-K-+
*-E-N-K-+
*-E-N-K-E-A-+
*-L-E-N-K-E-+
*-K-L-E-N-K-+
*-K-L-E-N-K-E-A-+
*-S-G-Q-+

*-N-Q-L-+
*-N-Q-L-I-K-+
*-N-Q-I-K-+
*-S-N-Q-L-+
*-S-N-Q-L-I-K-+
*-S-N-Q-I-K-+
*-N-S-N-Q-+
*-N-S-N-Q-L-I-+
*-N-S-N-Q-I-K-+

*-K-N-S-N-Q-+
*-K-N-S-N-Q-L-I-+
*-K-N-S-N-Q-I-+
*-N-S-N-Q-I-+
*-E-N-K-E-+
*-L-E-N-K-+
*-L-E-N-K-E-A-+
*-K-L-E-N-K-E-+

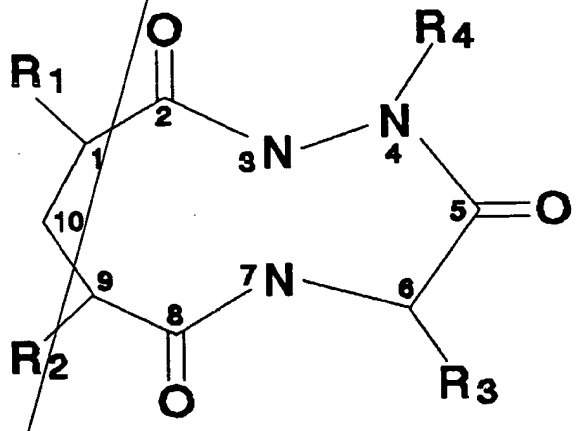
*-S-G-Q-V-+

*-S-G-Q-V-L-+
*-D-S-G-Q-V-+
*-S-D-S-G-Q-+
*-S-D-S-G-Q-V-L-+
*-L-S-D-S-G-Q-V-+ and

*-D-S-G-Q-+
*-D-S-G-Q-V-L-+
*-S-D-S-G-Q-V-+
*-L-S-D-S-G-Q-+
*-L-S-D-S-G-Q-V-L-+,

wherein * and + designate the amino and carboxyl termini, respectively, and the single letters designate L-amino acids according to the single letter code or wherein * and + designate the carboxyl and amino termini, respectively and the single letters designate D-amino acids according to the single letter code.

19. A method of suppressing a human, CD4 T-cell immune response comprising administering to a subject having a medical condition that is ameliorated by the suppression of a CD4 T-cell mediated immune response, an effective amount of a macrocyclic peptidomimetic corresponding to a tetrameric, pentameric or hexameric peptide, having a 10-member ring according to the formula:



wherein:

R_1 is the α-carbon, amino moiety and side chain of the amino terminal amino acid of a tetrameric peptidomimetic or the amino terminal amino acid and the α-carbon, amine and side chain of the second amino acid of a pentameric or hexameric peptidomimetic;

R_2 is the side-chain of the second amino acid of a tetrameric or pentameric peptidomimetic or the side-chain of the third amino acid of a pentameric or hexameric peptidomimetic;

R_3 is the side chain of the third amino acid of a tetrameric or pentameric peptidomimetic or the fourth amino acid of a pentameric or hexameric peptidomimetic; and

R_4 and 4-N together are the carboxyl terminal amino acid of a tetrameric or pentameric peptidomimetic, or the carboxyl terminal two amino acids of a pentameric or hexameric peptidomimetic; and

the sequence of amino acids to which R_1 through R_4 correspond are selected from the following sequences:

*-N-Q-L-I-+
*-N-Q-I-K-+
*-S-N-Q-L-I-+
*-S-N-Q-I-+
*-N-S-N-Q-+
*-N-S-N-Q-L-I-+
*-N-S-N-Q-I-+
*-K-N-S-N-Q-+
*-K-N-S-N-Q-I-+
*-N-S-N-Q-I-+
*-E-N-K-E-A-+
*-L-E-N-K-E-+
*-K-L-E-N-K-+
*-S-G-Q-V-+
*-D-S-G-Q-+
*-D-S-G-Q-V-L-+
*-S-D-S-G-Q-V-+ and
*-N-Q-L-I-K-+
*-S-N-Q-L-+
*-S-N-Q-L-I-K-+
*-S-N-Q-I-K-+
*-N-S-N-Q-L-+
*-N-S-N-Q-I-K-+
*-K-N-S-N-+
*-K-N-S-N-Q-L-+
*-E-N-K-E-+
*-L-E-N-K-+
*-L-E-N-K-E-A-+
*-K-L-E-N-K-E-+
*-S-G-Q-V-L-+
*-D-S-G-Q-V-+
*-S-D-S-G-Q-+
*-L-S-D-S-G-Q-+,

wherein * denotes the amino terminal and + the carboxyl terminal.